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FULL ESTIMATED COST	0.21	0.48

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=> s phbC and phbB and phbA and transform?

=> s phbC and phbB and phbA and pseudomonas
L3 9 PHBC AND PHBB AND PHBA AND PSEUDOMONAS

=> d l3 1-9 ibib ab

L3 ANSWER 1 OF 9 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation
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ACCESSION NUMBER: 1999:73797 BIOSIS

DOCUMENT NUMBER: PREV199900073797

TITLE: Cloning and molecular analysis of the poly(3-hydroxybutyrate) and poly(3-hydroxybutyrate-co-3-hydroxyalkanoate) biosynthesis genes in

Pseudomonas

sp. strain 61-3.

AUTHOR(S): Matsusaki, Hiromi; Manji, Sumihide; Taguchi, Kazunori;

Kato, Mikiya; Fukui, Toshiaki; Doi, Yoshiharu

[Reprint

author].

CORPORATE SOURCE: Polymer Chem. Lab., Inst. Phys. Chem. Res., 2-1
Hirosawa,

Wako-shi, Saitama 351-0198, Japan

SOURCE: Journal of Bacteriology, (Dec., 1998) Vol. 180, No.
24, pp.

6459-6467. print.

CODEN: JOBAAY. ISSN: 0021-9193.

DOCUMENT TYPE: Article

LANGUAGE: English

ENTRY DATE: Entered STN: 1 Mar 1999

Last Updated on STN: 1 Mar 1999

AB Two types of polyhydroxyalkanoate (PHA) biosynthesis gene loci (phb
and

pha) of ***Pseudomonas*** sp. strain 61-3, which produces a
blend of

poly(3-hydroxybutyrate) (P(3HB)) homopolymer and a random copolymer
(poly(3-hydroxybutyrate-co-3-hydroxyalkanoate) (P(3HB-co-3HA))

consisting

of 3HA units of 4 to 12 carbon atoms, were cloned and analyzed at

the

molecular level. In the phb locus, three open reading frames

encoding

polyhydroxybutyrate (PHB) synthase (PhbCPs), beta-ketothiolase

(PhbAPs),

and NADPH-dependent acetoacetyl coenzyme A reductase (PhbBPs) were
found.

The genetic organization showed a putative promoter region,
followed by

phbBPs-phbAPs-phbCPs. Upstream from phbBPs was found the phbRPs
gene,

which exhibits significant similarity to members of the AraC/XylS
family

of transcriptional activators. The phbRPs gene was found to be
transcribed in the opposite direction from the three structural

genes.

Cloning of phbRPs in a relatively high-copy vector in

Pseudomonas

sp. strain 61-3 elevated the levels of beta-galactosidase activity
from a

transcriptional phb promoter-lacZ fusion and also enhanced the 3HB
fraction in the polyesters synthesized by this strain, suggesting

=> s phbC and phbB and phbA
 L4 75 PHBC AND PHBB AND PHBA

=> duplicate remove l4
 DUPLICATE PREFERENCE IS 'AGRICOLA, BIOSIS, EMBASE, CAPLUS'
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PROCESSING COMPLETED FOR L4
 L5 51 DUPLICATE REMOVE L4 (24 DUPLICATES REMOVED)

=> d l5 1-10 ibib ab

L5 ANSWER 1 OF 51 CAPLUS COPYRIGHT 2005 ACS on STN
 ACCESSION NUMBER: 2004:906661 CAPLUS
 DOCUMENT NUMBER: 142:212974
 TITLE: Production of polyhydroxybutyrate by
 polycistronic expression of bacterial genes in tobacco
 plastid
 AUTHOR(S): Arai, Yuko; Shikanai, Toshiharu; Doi,
 Yoshiharu; Yoshida, Shigeo; Yamaguchi, Isamu; Nakashita,
 Hideo
 CORPORATE SOURCE: Microbial Toxicology Laboratory, Plant
 Functions Laboratory, RIKEN Institute, Wako, 351-0198,
 Japan
 SOURCE: Plant and Cell Physiology (2004), 45(9), 1176-
 1184
 CODEN: PCPHA5; ISSN: 0032-0781
 PUBLISHER: Japanese Society of Plant Physiologists
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB Transgenic techniques are used to enhance and improve crop prodn.,
 and their application to the prodn. of chem. resources in plants has
 been under investigation. To achieve this latter goal, multiple-gene
 transformation is required to improve or change plant metabolic
 pathways;
 when accomplished by plant nuclear transformation, however, this
 procedure is costly and time consuming. Authors succeeded in the metabolic
 engineering of the tobacco plant by introducing multiple genes
 within a bacteria-like operon into a plastid genome. A tobacco plastid was
 transformed with a polycistron consisting of the spectinomycin
 resistance gene and three bacterial genes for the biosynthesis of the
 biodegradable polyester, poly[(R)-3-hydroxybutyrate] (PHB), after modification of
 their ribosome binding sites. DNA and RNA anal. confirmed the insertion
 of the introduced genes into the plastid genome and their polycistronic
 expression. As the result, the transplastomic tobacco accumulated
 PHB in its leaves. The introduced genes and the PHB productivity were
 maternally inherited, avoiding genetic spread by pollen diffusion, and were
 maintained stably in the seed progeny. Despite the low PHB

=> s phbCAB

L6 63 PHBCAB

=> duplicate remove l6

DUPLICATE PREFERENCE IS 'AGRICOLA, BIOSIS, EMBASE, CAPLUS'

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PROCESSING COMPLETED FOR L6

L7 32 DUPLICATE REMOVE L6 (31 DUPLICATES REMOVED)

=> d 17 20-32 ibib ab

L7 ANSWER 20 OF 32 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation
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DUPLICATE 10

ACCESSION NUMBER: 2000:33419 BIOSIS

DOCUMENT NUMBER: PREV200000033419

TITLE: Acetate metabolism in a pta mutant of Escherichia coli

W3110: Importance of maintaining acetyl coenzyme A flux for growth and survival.

AUTHOR(S): Chang, Dong-Eun; Shin, Soan; Rhee, Joon-Shick; Pan, Jae-Gu

[Reprint author]

CORPORATE SOURCE: Bioprocess Engineering Division, Korea Research Institute

of Bioscience and Biotechnology (KRIBB), Yusong,

Taejon,

305-600, South Korea

SOURCE: Journal of Bacteriology, (Nov., 1999) Vol. 181, No. 21, pp.

6656-6663. print.

CODEN: JOBAAY. ISSN: 0021-9193.

DOCUMENT TYPE: Article

LANGUAGE: English

ENTRY DATE: Entered STN: 19 Jan 2000

Last Updated on STN: 31 Dec 2001

AB In order to study the physiological role of acetate metabolism in Escherichia coli, the growth characteristics of an E. coli W3100 pta

mutant defective in phosphotransacetylase, the first enzyme of the acetate

pathway, were investigated. The pta mutant grown on glucose

minimal

medium excreted unusual by-products such as pyruvate, D-lactate, and

L-glutamate instead of acetate. In an analysis of the sequential consumption of amino acids by the pta mutant growing in tryptone broth

(TB), a brief lag between the consumption of amino acids normally consumed

was observed, but no such lag occurred for the wild-type strain. The pta

mutant was found to grow slowly on glucose, TB, or pyruvate, but it grew

normally on glycerol or succinate. The defective growth and starvation

survival of the pta mutant were restored by the introduction of poly-beta-hydroxybutyrate (PHB) synthesis genes (***phbCAB***)

from

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<u>L5</u>	huisman-Gjalt-\$.in.	15	<u>L5</u>
<i>DB=USPT; PLUR=YES; OP=OR</i>			
<u>L4</u>	L1 and PHA and bacteria.clm.	12	<u>L4</u>
<u>L3</u>	L1 and PHA and bacteria	39	<u>L3</u>
<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>			
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<u>L1</u>	phbC and phbB and phbA and bacteria	61	<u>L1</u>

END OF SEARCH HISTORY